AMENDMENTS TO THE CLAIMS

Claims 1-56 (CANCELLED)

57. (New) A method of identifying a subject predisposed to small vessel occlusion, wherein said method comprises: identifying the presence of a thymine to cytosine mutation at position -107 in both alleles of the paraoxonase 1 locus, wherein the presence of the mutation in both alleles indicates the subject is predisposed to small vessel occlusion.

58. (New) The method according to claim 57, wherein the small vessel occlusion is a lacunar stroke, cerebral leukoaraiosis, dementia, ischemic heart disease including ischemic cardiomyopathy, peripheral vascular disease, disseminated intravascular coagulation, small vessel vasculitis, ischemic neuropathy, ischemic retinopathy, ischemic gastropathy including small and large bowel ischemia, diffuse pulmonary embolism, and vascular impotence.

59. (New) The method according to claim 57, wherein the small vessel occlusion occurs in the brain.

60. (New) The method according to claim 57, wherein the identification of the mutation comprises amplification of a region containing the mutation from nucleic acid isolated or derived from the subject.

61. (New) The method according to claim 57, wherein the identification of the mutation comprises detection of the mutation by hybridisation of nucleic acid isolated or derived from the subject to a reporter nucleic acid.

62. (New) The method according to claim 57, wherein the subject predisposed to small vessel occlusion is predisposed to developing a disease or condition associated with small vessel occlusion.

63. (New) The method according to claim 57, wherein the subject is suitable for treatment with an agent that decreases the activity of paraoxonase 1.

64. (New) A method of determining the risk of small vessel occlusion in a subject, wherein said method comprises: identifying the presence of a thymine to cytosine mutation at position -107 in one or both alleles of the paraoxonase 1 locus, wherein the presence of the mutation in both alleles indicates an increased risk that the subject is predisposed to small vessel occlusion.

65. (New) The method according to claim 64, wherein the risk of small vessel occlusion is compared to the risk of small vessel occlusion for a subject in the general population.

66. (New) The method according to claim 64, wherein the small vessel occlusion is a lacunar stroke, cerebral leukoaraiosis, dementia, ischemic heart disease comprising ischemic cardiomyopathy, peripheral vascular disease, disseminated intravascular coagulation, small

vessel vasculitis, ischemic neuropathy, ischemic retinopathy, ischemic gastropathy including small and large bowel ischemia, diffuse pulmonary embolism, and vascular impotence.

67. (New) The method according to claim 64, wherein the small vessel occlusion occurs in the brain.

68. (New) The method according to claim 64, wherein the identification of the mutation comprises amplification of a region containing the mutation from nucleic acid isolated or derived from the subject.

69. (New) The method according to claim 64, wherein the identification of the mutation comprises detection of the mutation by hybridisation of nucleic acid isolated or derived from the subject to a reporter nucleic acid.

70. (New) A method of preventing and/or treating a subject susceptible to a small vessel occlusion, the method including the step of administering to the subject an effective amount of an agent that decreases the activity of paraoxonase 1.

71. (New) The method according to claim 70, wherein the small vessel occlusion is a small vessel occlusion in the brain.

72. (New) The method according to claim 70, wherein the small vessel occlusion is a lacunar stroke, cerebral leukoaraiosis, dementia, ischemic heart disease including ischemic cardiomyopathy, peripheral vascular disease, disseminated intravascular coagulation, small vessel vasculitis, ischemic neuropathy, ischemic retinopathy, ischemic gastropathy including small and large bowel ischemia, diffuse pulmonary embolism, or vascular impotence.

73. (New) An isolated nucleic acid that (i) consists of the sequence according to SEQ. ID No.3 or SEQ ID NO.4, or a RNA equivalent thereof; or (ii) includes one or more base substitutions in the sequence according to SEQ ID No. 3 or SEQ ID NO.4, wherein the nucleic acid with one or more base substitutions has at least 80% homology to SEQ. ID No.3 or a RNA equivalent thereof; or (iii) includes one or more base substitutions in the sequence according to SEQ ID No. 3 or SEQ ID NO.4, wherein the nucleic acid with one or more base substitutions hybridises with the complement of SEQ ID No.3 under stringent hybridisation conditions and the stringent hybridisation conditions include hybridisation in 6xSSC at 42°C and washing in 2xSSC at 20°C.